

# Heartbeat Locations in the Ballistocardiographic Signal Sensor-A Method of Detecting

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**Abstract**—We present a flexible, easy-to-expand digital signal processing method for detecting heart rate (HR) for cardiac vibration signals of fiber Bragg grating (FBG) sensor. The FBG-based method of measuring HR is possible to use during the magnetic resonance imaging procedure, which is its unique advantage. Our goal was to design a detection method with plurality of parameters and to subject these parameters to genetic algorithm optimization technique. In effect, we arrived at a method that is well able to deal with much distorted signals with low SNR. We proved that the method we developed allows automatic adjustment to the shape of the waves of signal carrying useful information about the moments of heartbeat. Thus, we can easily adapt our technique to the analysis of signals, which contains information on HR, from sensors employing different techniques of strain detection. The proposed method has the capabilities of analyzing signals in semi-real-time (online) with beat-to-beat resolution, significantly low delay, and negligible computational power requirements. We verified our method on recordings in a group of seven subjects. Verification included over 6000 heartbeats (82 min 47 s of recordings). The root-mean-square error of our method does not exceed 6.0 bpm.

**Index Terms**—Ballistocardiographic (BCG) signal, fiber Bragg gratings (FBGs), genetic algorithms (GAs), heart rate (HR), parallel computing.

## I. INTRODUCTION

**H**EART rate (HR) is one of the fundamental physiological parameters, essential for the monitoring and diagnosis of patients. Some conditions, for example, a magnetic resonance imaging (MRI) environment, limit the use of conventional HR monitors due to their vulnerability to strong electromagnetic fields and the possibility of introducing interferences to the imaging [1]. However, the latest study [2] shows that HR trends may be crucial in predicting symptoms associated with claustrophobia, which often occurs in patients examined with the use of equipment limiting their movements such as MRI scanners [3]–[5]. In general, HR indicators are of considerably higher values in persons experiencing claustrophobic episodes, e.g., anxiety, panic, and hyperventilation, in comparison with those who do not experience such discomforts. Usually, already before a claustrophobic patient is placed inside the MRI tube, his/her HR values begin to rise and can reach dangerous levels during the examination. Therefore, continuous, online monitoring of trend changes in the patient's HR shortly before and during examination can be crucial in predicting and assessing

the possible occurrence of claustrophobia closely related to the circumstances of examination.

There are many other patient categories that require HR monitoring during MRI procedures, e.g., pediatric patients, disabled patients, sedated or anesthetized patients, critically-ill or high-risk patients, patients developing reactions to contrast media, as well as all patients who are unable or may not be able to communicate or to use the alarm button [6]. Contrary to the electronic transducers, fiber-optic sensors are immune to electromagnetic fields used in MRI, safe for the patient, and do not influence the imaging quality [7]–[10]. These advantages, together with the ability of the fiber-optic sensors to detect miniature deflections (e.g., those caused by heart-induced body movements), renewed the interest in recording ballistocardiographic (BCG) signal, [11], particularly in the context of patient monitoring during MRI examination [12].

Ballistocardiography has obvious advantages such as noninvasiveness, electrically contactless, as well as simple design of measurement systems. However, BCG signal analysis induces many problems. The main reason for this is the presence of motion artifacts in the measured signals. These artifacts are associated with the patient's body movements, as well as artifacts originating from the environment in applications such as examination of vehicle operators. The number of articles currently published considering the problem of BCG signal analysis [13]–[16] reveals the topicality and novelty of the subject.

## II. MEASUREMENT METHOD

The movements of the patient's body including the mechanical activity of the heart are the causes of force, pressure, and strain exerted on the sensing element. There are a number of fiber-optic strain gauges designed to monitor vital signs, of which the most popular are interferometers [17], micro- [10]–[11] and macrobending sensors [18], and fiber Bragg gratings (FBGs) [18], [19]. Many researchers took a liking to the FBGs due to their spectral encoding, easy multiplexing, and self-referencing capabilities [20]. The authors have used the in-house constructed FBG-based sensor to acquire BCG signal from an MRI patient's body [19]. Fig. 1(a) shows a photograph of the sensor; an elastic Plexiglas board with bonded FBG element is placed on the MRI couch behind the back of the patient close

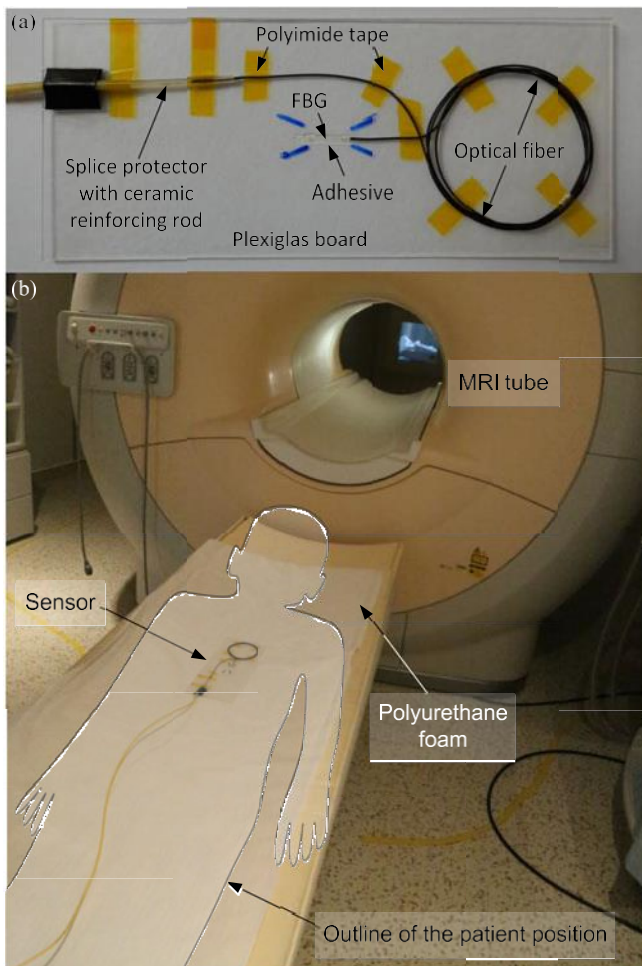


Fig. 1. Photograph of (a) fiber-optic vital signs sensor and (b) sensor in the MRI system.

to the heart as shown in Fig. 1(b). The Plexiglas board is of 209 cm<sup>2</sup> in area and as thin as 1.5 mm and can follow the contour of the body fragment when the patient lies on it. At the time, the FBG element is subjected to be strained due to body movements including those induced by heartbeats. Thus, the board is a medium reflecting body movements and converting them into strains (elongations/contractions) measurable by the FBG. A thin layer of epoxy adhesive is applied over the entire length of the grating. This protects the bare fiber against moisture and enables for transmitting strains to the FBG.

It has been demonstrated that the level of heart-induced strains is much less than the physical strength of the sensor [7], i.e., 8000  $\mu\epsilon$  [8]. Other body movements, e.g., sudden sneezes or coughs [9], as well as jerks of the MRI track table [19] do not pose a threat to the sensor, as the Plexiglas board is protected against large deformations by the hardness of the MRI couch, on which only a thin layer (~1 cm) of soft polyurethane foam is put to ensure comfort for the patient and allow the board to bend.

A Bragg grating can be considered as a frequency filter [21]. Depending on the measuring system, maximum or minimum attenuation of this filter occurs for signals with the resonant

frequency that depends on the grating period  $\Lambda$  [9] modulated by strains transmitted by the board to the FBG [9]. The value of the resonant frequency is measured by an interrogation system. We used an sm130-700 instrument manufactured by Micron Optics [22]; this is an optical scanner of frequency with a function of automatic seeking resonant frequency of the grating. A band of 1510–1590 nm was scanned 1000 times per second with the peak-to-peak resolution of 1 pm. The instantaneous spectral value of the resonant frequency of the FBG-based sensor can be calibrated in terms of heartbeat readings. Due to the so-called self-reference capability of FBGs, i.e., a return to the referential values of spectral parameters after achieving the initial conditions [23], the sensor does not require additional calibration.

The mechanical activity of the heart modulates the resonant frequency, but the cardiac activity is only one of the several sources of strains exerted on the FBG, such as respiration, any other body movements, or displacement of the track table during the MRI scanning process [7]. Therefore, we have developed a method to extract the heart-induced artifacts in the sensor signal as well as to provide moments of their occurrence. This allows determining a series of heartbeat time intervals (i.e., tachogram) and consequently, monitor the HR trace.

### III. DETECTION METHOD

The proposed technique uses signals from the sensor, in which the measurand is represented by means of wavelength readings rather than frequency readings. The wavelength domain is the most common way of analyzing the response of an FBG subjected to strain [12]. Thus, the Bragg wavelength value outlines the BCG signal shape as shown in Fig. 2. The peak of ventricular ejection phase exerts the greatest strain on the sensor, which appears in the ballistocardiogram as a series of the J wave peaks [24], [25], indicated by arrows in Fig. 2. The relatively high value of noise with respect to the values of the signal presented in Fig. 2 is the result of the resolution of the interrogator system which is 1 pm while usable peak-to-peak values of the signal are about 6 pm.

#### A. Detection Function

For detecting heartbeat positions, a specially prepared signal of the detection function is analyzed rather than the source signal from the sensor. The detection function enhances the signal characteristics associated with the heartbeats. The trace of the detection function is determined by software implementing a cascade of digital filters. Band-pass filter, quadratic function, and low-pass filter in this sequence are used [26], [27].

By using the aforementioned procedure, the algorithm avoids errors introduced by the impulse noise and fluctuations in the level of the signals originating from the stopband of filters. This approach also allows adjusting the characteristics of the filters to the shape of the signal characteristic waves corresponding to the heartbeats and thus, to the spectrum of the analyzed signal. Therefore, the same algorithm can be adapted for analyzing amplitude-modulated BCG signals originating from sensors employing different measurement methods (e.g., electromechanical films or piezoelectric transducers) [28]. The parameters of

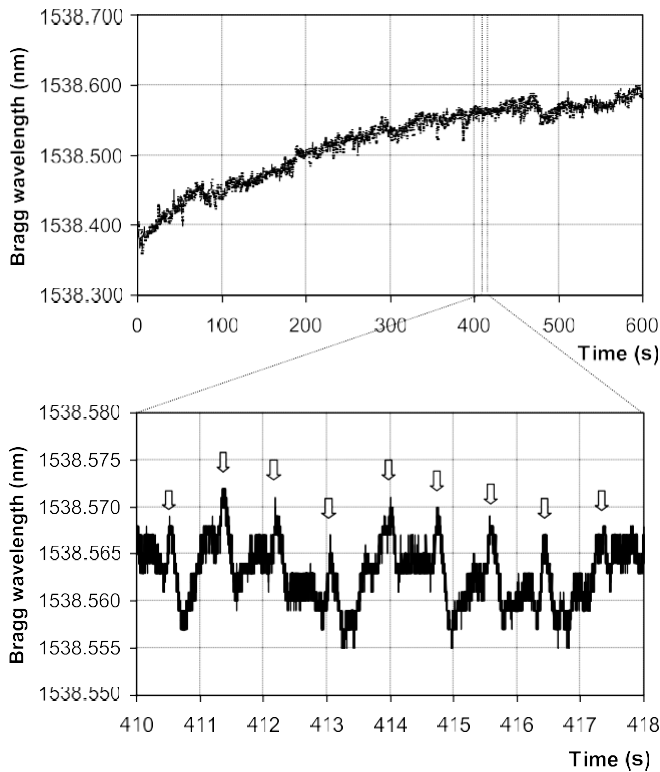


Fig. 2. Example of the input signal for the detection method.

the utilized filters are part of a set of values being subjected to the optimization process.

### B. Detecting Local Maxima

The next step of operation of the detection algorithm is to determine the time of occurrence of the local extremes in the signal, which may potentially be used as the characteristic moments sourced by the heart. A given value of the signal is classified by the algorithm as a potential distinctive moment if it is the maximum value of the signal for the time interval whose center falls at the time of this value. The width of this interval is one of the parameters of the algorithm being part of the set of values subjected to the optimization. Fig. 3 shows a portion of the detection function signal with examples of markers set at the positions of the found maxima (yellow) and markers of maxima classified as characteristic moments (green). The frames indicate widths of the maxima search windows.

For each subsequent sample of the signal, it is verified whether it occurs in the characteristic time. This verification is based on the analysis of samples in two windows of the same size: 1) a window preceding the analyzed sample; and 2) a window that follows after the sample. We assume that the searched sample is an extreme if the maximum values for both windows fall on the mutual point.

### C. Correcting Local Maxima Series

In the later stage of the method, algorithms improving the sequence of the potential characteristic moments are applied.

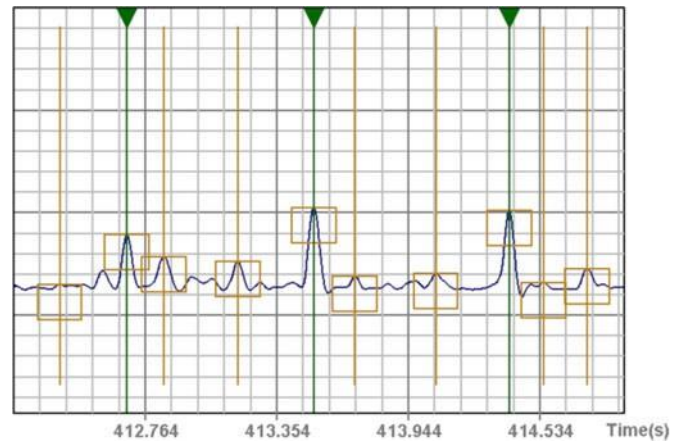


Fig. 3. Examples of markers set at the found maxima.

These algorithms, hereinafter referred to as the correctors, are interchangeable and customizable elements of the processing. A number of correctors have been developed. In the field of software engineering, these correctors have been implemented as a system of decorator classes [29]. Each corrector receives the incoming stream of maxima, processes them, and sends the output of the processed extremes stream. This processing may involve both generation and filtering of the maxima. The proposed method is capable of analyzing the signal online. The design comprises a chain of correctors; each of them that independently processes the stream of items is determined by the requirement of the method's ability to act as a semi-real-time digital signal processing element. The presented approach employs the following correctors:

- 1) classifying corrector,
- 2) averaging corrector, and
- 3) corrector of gaps.

1) *Classifying Corrector*: The corrector accumulates the incoming stream of times of local maxima from the time range with a specified width. This width belongs to the parameters that are the subject of optimization. Then, a set of values identifying a potential imperfection of the maxima for each of the collected extremes is assigned. Subsequently, these characteristics are multiplied by a set of weights selected in the optimization process, and summed. The classifier selects the maximum with the lowest cumulative imperfection and forwards it for further processing.

Designation of many of these features depends on the value of the  $JJ$  interval. This value is defined as the interval between the analyzed center of the wave,  $t_n$ , and the former one,  $t_{n-1}$  classified as artifact derived from the heartbeat, i.e., ventricular ejection, given by

$$JJ_n = t_n - t_{n-1}. \quad (1)$$

The following features of the incoming maxima are determined by the classifying corrector.

- 1) The ratio of the local maximum value to the average of  $N$  previously selected local maxima values, where  $N$  is the parameter subjected to optimization.

- 2) The ratio of the  $JJ$  interval of the current maximum to the average  $JJ$  interval between  $M$  selected earlier extremes, where  $M$  is the parameter subjected to optimization.
- 3) The current  $JJ$  interval, used to prevent unnecessary skipping of the maxima, although the share of such behavior through a system of weights is selected by optimization.
- 4) The current interval length exceeding beyond the acceptable range. We assumed the value of 0.25 s (HR = 240 bpm) as the minimum of the interval and the value of 2 s (HR = 30 bpm) as the maximum of the interval. This range is intentionally wider than what is generally used in the physiology.
- 5) Deviation of values of consecutive intervals,  $\Delta JJ_n = |J_n - J_{n-1}|$ , beyond the acceptable range ( $\Delta JJ_{\max} = 30\text{bpm}$ ).
- 6) The value of relative change of consecutive intervals,  $\delta_{JJ_n}$ , given by

$$\delta_{JJ_n} = \frac{|JJ_n - JJ_{n-1}|}{JJ_n} \quad (2)$$

2) *Averaging Corrector*: This corrector involves replacing the position of maximum  $t_n$  with the center of positions of its neighbors according to

$$\bar{t}_n = \frac{t_{n+1} + t_{n-1}}{2} \quad (3)$$

From the stream of incoming maxima, these are modified, for which the value of relative change of consecutive intervals,  $\delta_{JJ_n}$ , determined according to (2), exceeds the limit parameter. This parameter is also included in the set of values subjected to optimization.

3) *Corrector of Gaps*: The purpose of the next corrector is to fill the gaps appearing in the detected maxima stream. Similar to the averaging corrector, the logic of the corrector of gaps is sensitive to relative change of consecutive intervals,  $\delta_{JJ_n}$ , determined according to (2), exceeding the limit parameter, which is also a part of the set of values subjected to optimization. The second value, which is observed by the corrector, is the HR and the fact that its value exceeds the acceptable range (similar to the classification corrector). Exceeding the limit values in the incoming stream of maxima is regarded as the beginning of the gap. The return of parameters to the acceptable ranges means the end of the gap.

The given time of a detected gap is analyzed to detect a new set of heartbeat positions. The first task of the algorithm detecting position of gaps is to search local maxima with a narrow window, i.e., 0.1 s. Narrow windows generate large sets of maxima. This logic comes down to analysis of an array of detected local maxima to find a new set of characteristic wave centers that will fill the given gap. The number of positions to insert is the input variable of a procedure, which aims to find the potential set of new maxima dividing a gap.

In subsequent stage, the number of positions for inserting is increased by 1 from 1 until it reaches the value equal to the total number of available extremes. For each number of the positions to insert, the set of maxima dividing gap is determined, and then the variability of the HR signal corresponding to a given layout

is calculated. The algorithm looks for a layout of maxima, which corresponds to the smallest variability of the HR signal.

The procedure of finding a set of extremes filling a gap with a given number of positions in the first step divides the gap into subranges of equal length. Then, in the array of previously found maxima, the positions nearest to the edges of subranges are searched. In the following steps, each maximum in the set is replaced by the maximum nearest to the averaged time of its closest neighbor maxima. This operation is repeated multiple times until the system of chosen maxima ceases to change.

#### D. Optimization

For optimizing the parameters of the detection method, the genetic algorithm (GA) has been implemented. In the implementation of this method, a .Net platform and C# programming language have been applied. The reason was the possibility of using the computing power of the grid of multicore computers.

Along with version 4 of the .Net platform, parallel computing library *Microsoft Parallel Extensions (PFX)* was introduced

[30]. This is a managed library of parallelization of tasks. Its basic elements are *Parallel LINQ (PLINQ)* and *Task Parallel Library (TPL)*. *PLINQ* supports data parallelism wherein the set of tasks is executed simultaneously on the different subranges of data. The method of implementation is based on the technique of integrated query language, *LINQ*. *TPL* supports task parallelism and provides parallelized versions of the *ForEach* and *For* loops. The library supports the user in tasks such as management of threads of operating system used to perform calculations.

The idea of GAs has been derived from the theory of evolution. The techniques inspired by natural phenomena are, in particular, mutation, inheritance, selection, and crossing. In a GA, the population (i.e., a set of solutions) stored as a sequence of genes (genome), evolves toward better solutions pointed by the fitness function [31].

In the presented approach, the objective of the optimization is finding an optimal set of parameters of heartbeat detection method, which analyzes signals coming from the FBG-based sensor. The set of these variables creates a virtual genome. The most common way to represent variables in the genome is binary encoding. It is a natural coding method for integer parameters. For values that have the nature of real numbers, quantization or bit representations of floating point numbers can be applied. In the presented optimization problem, some variables are integers, and some are real numbers. Due to the predominance of the parameters stored as real numbers, direct floating point representation of parameters has been applied. This means that the described variation of the evolutionary algorithm represents real-valued GA [32].

During the search for the optimal solution with the use of evolutionary algorithms for each individual genome of population, fitness function is computed for determining the probability of reproduction. The choice of individuals who will participate in the reproduction is the selection process. There are several known selection schemes. In the presented implementation, stochastic remainder selection without replacement has been applied [33]. Assuming that the expected number of

TABLE I  
RESULTS OF EVALUATION OF THE PROPOSED METHOD

Subject no.	1	2	3	4	5	6	7	8	Total
Rec. time (min:s)	9:34	10:52	10:48	10:26	10:42	10:43	9:49	9:54	82:47
Beats count	783	748	793	645	776	675	587	1087	6094
Mean HR (bpm)	82.3	69.0	73.4	62.3	72.6	63.2	59.8	110.0	76.8
SD (bpm)	6.6	4.7	4.3	6.6	4.7	5.3	3.6	6.7	17.7
RMSE (bpm)	6.7	4.8	3.2	4.8	2.9	5.9	3.9	9.7	6.0
RMS of relative error (%)	8.2	6.7	8.1	7.6	4.1	9.9	6.2	7.1	7.4
Mean error; bias (bpm)	-1.4	-0.5	-0.3	0.1	-0.3	-0.8	-0.4	-0.9	-0.6

TABLE II  
PARAMETERS SUBJECTED TO OPTIMIZATION AND THEIR OPTIMAL VALUES

Parameter	Optimal value
Low cutoff frequency of band pass filter	4.72491 Hz
High cutoff frequency of band pass filter	29.51572 Hz
Cutoff frequency of low-pass bass filter	6.93891 Hz
Half-width of the window of local maxima detection algorithm	0.185 s
Width of interval of which the classifying corrector selects local maxima for comparison	4.8 s
Number of values of maxima, $N$ , averaged for estimation a feature (a) of maximum determined by classifying corrector	19
Number of intervals, $M$ , averaged for estimation a feature (b) of maximum determined by classifying corrector	13
Weight for component (a) criterion for classifying corrector	4.42746
Weight for component (b) criterion for classifying corrector	4.68384
Weight for component (c) criterion for classifying corrector	0.83594
Weight for component (d) criterion for classifying corrector	0.37800
Weight for component (e) criterion for classifying corrector	7.41111
Weight for component (f) criterion for classifying corrector	9.21850
Limit value of relative change of consecutive intervals, $\delta_{Jm}$ , of averaging corrector	0.1515
Limit value of relative change of consecutive intervals, $\delta_{Jm}$ , of corrector of gaps	1.0687

copies of each solution,  $e_i$ , is given by

$$e_i = \frac{f_i}{\sum_{j=1}^P f_j} \quad (4)$$

where  $f_i$  is the value of fitness of  $i$ th genome, and  $P$  is the number of genomes in population. In this selection scheme, each individual is copied as many times as is the integer part of  $e_i$ . The fractional part of  $e_i$  is the probability of selection of an individual one more time.

The creation of the descendants of individuals of the population relies on crossing their genomes. Special variants of the arithmetic crossing operation are proposed for the GA [31], wherein the genes of the descendants,  $z_1$ , and,  $z_2$ , are the sum of ancestral genes  $x$  and  $y$  according to

$$z_1 = x(1 - \alpha) + y(\alpha) \quad (5)$$

$$z_2 = x(\alpha) + y(1 - \alpha) \quad (6)$$

where  $\alpha: 0 \leq \alpha \leq 1$ .

However, the performed tests have shown that discrete crossing operation (i.e.,  $\alpha = 1$  or  $\alpha = 0$ ) with one crossing point is best suited for the applied configuration of GA.

Given two parents  $\{x_1, x_2, \dots, x_n\}$  and  $\{y_1, y_2, \dots, y_n\}$ , split point position,  $k$ , is picked stochastically. Then, the first of the descendants will take the form (7), and the other one will take the form (8)

$$\{x_1, x_2, \dots, x_{k-1}, y_k, \dots, y_n\} \quad (7)$$

$$\{y_1, y_2, \dots, y_{k-1}, x_k, \dots, x_n\}. \quad (8)$$

Another important mechanism of GA is mutation. Mutation is one of the ways to maintain genetic diversity of a population, which enables one to avoid premature convergence of the algorithm. Mutation involves the introduction of random gene values into the population. It is carried out with a certain probability, which is a very important GA parameter. We used mutation operator based on a standard normal distribution and we applied a probability of mutation equal to 0.05.

In the presented GA application, scaling of the fitness function was also applied. We used linear scaling and sigma truncation. Linear scaling prevents premature convergence of a population to one of the local maxima, which can result in overlooking the global maximum. The idea of scaling is based on a linear transformation of fitness given by

$$f^j = af + b \quad (9)$$

where  $a$  and  $b$  are the values selected so as the fitness of the best individuals is scaled into the mean fitness of population multiplied by an empirically chosen factor. At the same time, the fitness value of average individuals remains unchanged. In typical applications, the multiplication factor is a number of the range 1.2 to 2; we assumed the value of 2.

To avoid problems with negative values of fitness function, linear scaling was preceded by sigma truncation scaling, in which the primary value of fitness function is moved toward lower values according to

$$f^j = f - \bar{f} + c\sigma \quad (10)$$

where  $c$  is a number of the range 1–3,  $\bar{f}$  is the average value of fitness of population, and  $\sigma$  is the standard deviation of fitness of population; we assumed  $c$  to be equal to 2.

An important aspect of the optimization using GAs is also the fitness function. Often, this function cannot directly constitute one of the indicators describing the objective of optimization. The fitness has limitations such as nonnegativity and growth toward better solutions.

After a series of tests, we have developed the following procedure of determining the base coefficient of fitness function,  $I_e$ . Both irregularly sampled HR signals, that is, one subjected to analysis and the reference signal, are interpolated; the integral of absolute difference of these signals is determined according to

$$I_e = \int_0^T |HR(t) - HR_{ref}(t)| dt \quad (11)$$

where  $T$  is the duration of the signal.

In practice, a numerical approximation of the previous integral is computed. For this purpose, both the interpolated signals are equally sampled at a frequency of 10 Hz. Finally, the value of fitness function is determined as follows:

$$f = \max \left( 0, 1 - \frac{\ln(1 + I_e)}{\ln(1 + CT)} \right) \quad (12)$$

where  $C$  is a constant equal to 60 bpm.

Due to the use of filtration as an element of the detection method and subjecting the filter parameters to the optimization process, it is necessary to design the digital filter in the process of calculations. For this purpose, we used an analytical software package *Matlab* with *Matlab Builder NE* toolbox, which allowed the integration of components developed in *Matlab* with application created for the *.Net* platform.

The dataset used in the optimization included nine 5-min registrations in a group of six male and three female subjects. The study was conducted in stationary conditions. The examined subjects were sitting on a chair with a sensor placed on the back seat. An ECG recorder was used during the study to determine the reference positions of heartbeats. Optimization was performed using a population of 64 genomes. A full list of variables subjected to optimization with their optimal values is presented in Table I.

Calculations were performed on three Intel Core i7-2600 processor computers with four cores, i.e., eight threads, each. The genome chosen for verification was obtained in 701 generation after 42 h of computation.

#### IV. VERIFICATION

A verification study was carried out on a group of eight subjects (six males and two females). Each of the experiments included simultaneous recording of the FBG sensor-based signal and ECG signal. The reference positions of heartbeats were determined from the R waves of ECG. Verification included over 6000 heartbeats. The total acquisition time was 82 min 47 s.

Table II shows the root-mean-square error (RMSE) for each study separately as well as other performance indexes of the algorithm, including root-mean-square (RMS) of relative error. The RMSE reached a value of 6.0 bpm corresponding to RMS of relative error ratio of 7.4%.

Proposed method (black) and compared with the reference HR (gray).

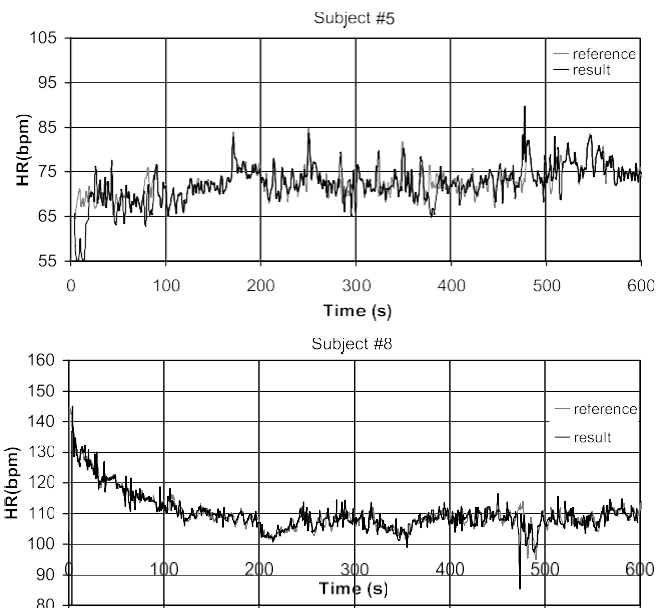


Fig. 4. Example of the HR traces obtained in subjects #5 and #8 using the

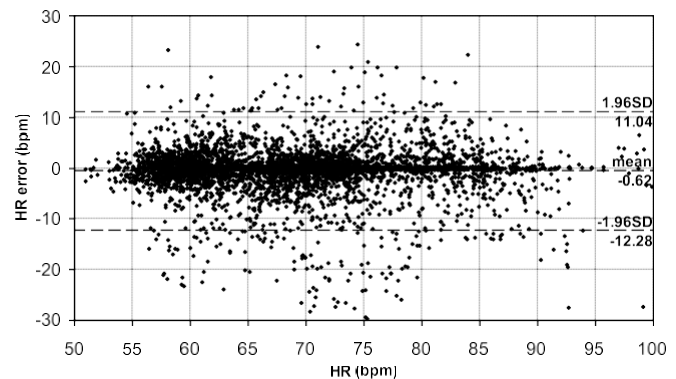


Fig. 5. Bland–Altman plot for the obtained HR samples.

Fig. 4 shows an example of a comparison of HR signals obtained from a recording in subjects #5 and #8, with the reference HR signal. Most of the time, the signals being compared overlap; however, in certain moments, the differences occur due to faults of the method, which are caused by movement artifacts in the source signal.

The analysis of accuracy of the method was made using the Bland–Altman plot shown in Fig. 5, in which the differences between gained HR values and the reference signal values are plotted against their averages. The confidence interval for the error of the method is  $\langle -12.28 \text{ bpm}; 11.04 \text{ bpm} \rangle$  with a mean error of  $-0.62 \text{ bpm}$ . The graph shows no significant correlation of errors with the HR; in addition, bias of the method is negligibly small. Concentration of points in the lower range of the HR values results from greater number of samples obtained in this range.

#### V. CONCLUSION

We have reported a method for detecting the HR trace from the BCG signal acquired by the MRI-compatible fiber-optic sensor.

The detection of heartbeat location in the ballistocardiogram is a complex task, mainly due to small levels of the useful waveform amplitude in the source signal in relation to the noise and resolution of the measurement system. According to the previously reported results, the authors estimate the signal-to-noise ratio at 3.37 dB [19]. At the same time, the usable peak-to-peak values are approximately 6 pm, whereas the resolution of the interrogation system is 1 pm. Nevertheless, the proposed method for establishing the detection procedure with multiple parameters subjected to optimization allowed us to achieve satisfactory results for the automatic detection of heartbeat positions.

The method, due to its flexible design, is easy to expand, in particular, for the ability to add correctors easily. Currently, we are considering supplementing the method with a Bayesian classifier corrector, described by Brüser *et al.* [16]. Future work will also include the adaptation of the method to the development of a sensor system based on a matrix of FBGs. This feature will enable signal acquisition from multiple body locations and thus improve the measurement reliability.

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